

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/S82, S08
Source: IFWP
Date Processed by STIC: 6/28/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/582,508

CRF Edit Date: 6/28/06
Edited by: ZCE

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☒ Deleted: ☒ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFWP

RAW SEQUENCE LISTING

DATE: 06/28/2006

PATENT APPLICATION: US/10/582,508

TIME: 14:50:12

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06282006\J582508.raw

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3 <110> APPLICANT: Hisamitsu Pharmaceutical Co., Inc.; Chiba-Prefecture
5 <120> TITLE OF INVENTION: Method for Determining Clinical Severity of FALS
7 <130> FILE REFERENCE: FP04-0444-00WO-HM
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/582,508
C--> 10 <141> CURRENT FILING DATE: 2006-06-09
12 <150> PRIOR APPLICATION NUMBER: JP 2003-413629
13 <151> PRIOR FILING DATE: 2003-12-11
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1585
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <223> OTHER INFORMATION:
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28 Met Ala Ser Pro Ser Arg Asn Ser Gln Ser Arg Arg Arg Cys Lys Glu
29 1 5 10 15
31 Pro Leu Arg Tyr Ser Tyr Asn Pro Asp Gln Phe His Asn Met Asp Leu
32 20 25 30
34 Arg Gly Gly Pro His Asp Gly Val Thr Ile Pro Arg Ser Thr Ser Asp
35 35 40 45
37 Thr Asp Leu Val Thr Ser Asp Ser Arg Ser Thr Leu Met Val Ser Ser
38 50 55 60
40 Ser Tyr Tyr Ser Ile Gly His Ser Gln Asp Leu Val Ile His Trp Asp
41 65 70 75 80
43 Ile Lys Glu Glu Val Asp Ala Gly Asp Trp Ile Gly Met Tyr Leu Ile
44 85 90 95
46 Asp Glu Val Leu Ser Glu Asn Phe Leu Asp Tyr Lys Asn Arg Gly Val
47 100 105 110
49 Asn Gly Ser His Arg Gly Gln Ile Ile Trp Lys Ile Asp Ala Ser Ser
50 115 120 125
52 Tyr Phe Val Glu Pro Glu Thr Lys Ile Cys Phe Lys Tyr Tyr His Gly
53 130 135 140
55 Val Ser Gly Ala Leu Arg Ala Thr Thr Pro Ser Val Thr Val Lys Asn
56 145 150 155 160
58 Ser Ala Ala Pro Ile Phe Lys Ser Ile Gly Ala Asp Glu Thr Val Gln
59 165 170 175
61 Gly Gln Gly Ser Arg Arg Leu Ile Ser Phe Ser Leu Ser Asp Phe Gln
62 180 185 190
64 Ala Met Gly Leu Lys Lys Gly Met Phe Phe Asn Pro Asp Pro Tyr Leu
65 195 200 205
67 Lys Ile Ser Ile Gln Pro Gly Lys His Ser Ile Phe Pro Ala Leu Pro

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PATENT APPLICATION: US/10/582,508

DATE: 06/28/2006

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Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06282006\J582508.raw

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68      210      215      220
70 His His Gly Gln Glu Arg Arg Ser Lys Ile Ile Gly Asn Thr Val Asn
71 225      230      235      240
73 Pro Ile Trp Gln Ala Glu Gln Phe Ser Phe Val Ser Leu Pro Thr Asp
74      245      250      255
76 Val Leu Glu Ile Glu Val Lys Asp Lys Phe Ala Lys Ser Arg Pro Ile
77      260      265      270
79 Ile Lys Arg Phe Leu Gly Lys Leu Ser Met Pro Val Gln Arg Leu Leu
80      275      280      285
82 Glu Arg His Ala Ile Gly Asp Arg Val Val Ser Tyr Thr Leu Gly Arg
83      290      295      300
85 Arg Leu Pro Thr Asp His Val Ser Gly Gln Leu Gln Phe Arg Phe Glu
86 305      310      315      320
88 Ile Thr Ser Ser Ile His Pro Asp Asp Glu Glu Ile Ser Leu Ser Thr
89      325      330      335
91 Glu Pro Glu Ser Ala Gln Ile Gln Asp Ser Pro Met Asn Asn Leu Met
92      340      345      350
94 Glu Ser Gly Ser Gly Glu Pro Arg Ser Glu Ala Pro Glu Ser Ser Glu
95      355      360      365
97 Ser Trp Lys Pro Glu Gln Leu Gly Glu Gly Ser Val Pro Asp Arg Pro
98      370      375      380
100 Gly Asn Gln Ser Ile Glu Leu Ser Arg Pro Ala Glu Glu Ala Ala Val
101 385      390      395      400
103 Ile Thr Glu Ala Gly Asp Gln Gly Met Val Ser Val Gly Pro Glu Gly
104      405      410      415
106 Ala Gly Glu Leu Leu Ala Gln Val Gln Lys Asp Ile Gln Pro Ala Pro
107      420      425      430
109 Ser Ala Glu Glu Leu Ala Glu Gln Leu Asp Leu Gly Glu Glu Ala Ser
110      435      440      445
112 Ala Leu Leu Leu Glu Asp Gly Glu Ala Pro Ala Ser Thr Lys Glu Glu
113      450      455      460
115 Pro Leu Glu Glu Glu Ala Thr Thr Gln Ser Arg Ala Gly Arg Glu Glu
116 465      470      475      480
118 Glu Glu Lys Glu Gln Glu Glu Glu Gly Asp Val Ser Thr Leu Glu Gln
119      485      490      495
121 Gly Glu Gly Arg Leu Gln Leu Arg Ala Ser Val Lys Arg Lys Ser Arg
122      500      505      510
124 Pro Cys Ser Leu Pro Val Ser Glu Leu Glu Thr Val Ile Ala Ser Ala
125      515      520      525
127 Cys Gly Asp Pro Glu Thr Pro Arg Thr His Tyr Ile Arg Ile His Thr
128      530      535      540
130 Leu Leu His Ser Met Pro Ser Ala Gln Gly Gly Ser Ala Ala Glu Glu
131 545      550      555      560
133 Glu Asp Gly Ala Glu Glu Glu Ser Thr Leu Lys Asp Ser Ser Glu Lys
134      565      570      575
136 Asp Gly Leu Ser Glu Val Asp Thr Val Ala Ala Asp Pro Ser Ala Leu
137      580      585      590
139 Glu Glu Asp Arg Glu Glu Pro Glu Gly Ala Thr Pro Gly Thr Ala His
140      595      600      605

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Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06282006\J582508.raw

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142 Pro Gly His Ser Gly Gly His Phe Pro Ser Leu Ala Asn Gly Ala Ala
143      610                      615                      620
145 Gln Asp Gly Asp Thr His Pro Ser Thr Gly Ser Glu Ser Asp Ser Ser
146 625                      630                      635                      640
148 Pro Arg Gln Gly Gly Asp His Ser Cys Glu Gly Cys Asp Ala Ser Cys
149                      645                      650                      655
151 Cys Ser Pro Ser Cys Tyr Ser Ser Ser Cys Tyr Ser Thr Ser Cys Tyr
152                      660                      665                      670
154 Ser Ser Ser Cys Tyr Ser Ala Ser Cys Tyr Ser Pro Ser Cys Tyr Asn
155                      675                      680                      685
157 Gly Asn Arg Phe Ala Ser His Thr Arg Phe Ser Ser Val Asp Ser Ala
158      690                      695                      700
160 Lys Ile Ser Glu Ser Thr Val Phe Ser Ser Gln Asp Asp Glu Glu Glu
161 705                      710                      715                      720
163 Glu Asn Ser Ala Phe Glu Ser Val Pro Asp Ser Met Gln Ser Pro Glu
164                      725                      730                      735
166 Leu Asp Pro Glu Ser Thr Asn Gly Ala Gly Pro Trp Gln Asp Glu Leu
167                      740                      745                      750
169 Ala Ala Pro Ser Gly His Val Glu Arg Ser Pro Glu Gly Leu Glu Ser
170                      755                      760                      765
172 Pro Val Ala Gly Pro Ser Asn Arg Arg Glu Gly Glu Cys Pro Ile Leu
173      770                      775                      780
175 His Asn Ser Gln Pro Val Ser Gln Leu Pro Ser Leu Arg Pro Glu His
176 785                      790                      795                      800
178 His His Tyr Pro Thr Ile Asp Glu Pro Leu Pro Pro Asn Trp Glu Ala
179                      805                      810                      815
181 Arg Ile Asp Ser His Gly Arg Val Phe Tyr Val Asp His Val Asn Arg
182                      820                      825                      830
184 Thr Thr Thr Trp Gln Arg Pro Thr Ala Ala Ala Thr Pro Asp Gly Met
185      835                      840                      845
187 Arg Arg Ser Gly Ser Ile Gln Gln Met Glu Gln Leu Asn Arg Arg Tyr
188      850                      855                      860
190 Gln Asn Ile Gln Arg Thr Ile Ala Thr Glu Arg Ser Glu Glu Asp Ser
191 865                      870                      875                      880
193 Gly Ser Gln Ser Cys Glu Gln Ala Pro Ala Gly Gly Gly Gly Gly Gly
194                      885                      890                      895
196 Gly Ser Asp Ser Glu Ala Glu Ser Ser Gln Ser Ser Leu Asp Leu Arg
197                      900                      905                      910
199 Arg Glu Gly Ser Leu Ser Pro Val Asn Ser Gln Lys Ile Thr Leu Leu
200      915                      920                      925
202 Leu Gln Ser Pro Ala Val Lys Phe Ile Thr Asn Pro Glu Phe Phe Thr
203      930                      935                      940
205 Val Leu His Ala Asn Tyr Ser Ala Tyr Arg Val Phe Thr Ser Ser Thr
206 945                      950                      955                      960
208 Cys Leu Lys His Met Ile Leu Lys Val Arg Arg Asp Ala Arg Asn Phe
209                      965                      970                      975
211 Glu Arg Tyr Gln His Asn Arg Asp Leu Val Asn Phe Ile Asn Met Phe
212                      980                      985                      990
214 Ala Asp Thr Arg Leu Glu Leu Pro Arg Gly Trp Glu Ile Lys Thr Asp

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/582,508

DATE: 06/28/2006

TIME: 14:50:12

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06282006\J582508.raw

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215          995          1000          1005
217 Gln Gln Gly Lys Ser Phe Phe Val Asp His Asn Ser Arg Ala Thr Thr
218      1010          1015          1020
220 Phe Ile Asp Pro Arg Ile Pro Leu Gln Asn Gly Arg Leu Pro Asn His
221 1025          1030          1035          1040
223 Leu Thr His Arg Gln His Leu Gln Arg Leu Arg Ser Tyr Ser Ala Gly
224          1045          1050          1055
226 Glu Ala Ser Glu Val Ser Arg Asn Arg Gly Ala Ser Leu Leu Ala Arg
227      1060          1065          1070
229 Pro Gly His Ser Leu Val Ala Ala Ile Arg Ser Gln His Gln His Glu
230      1075          1080          1085
232 Ser Leu Pro Leu Ala Tyr Asn Asp Lys Ile Val Ala Phe Leu Arg Gln
233 1090          1095          1100
235 Pro Asn Ile Phe Glu Met Leu Gln Glu Arg Gln Pro Ser Leu Ala Arg
236 1105          1110          1115          1120
238 Asn His Thr Leu Arg Glu Lys Ile His Tyr Ile Arg Thr Glu Gly Asn
239      1125          1130          1135
241 His Gly Leu Glu Lys Leu Ser Cys Asp Ala Asp Leu Val Ile Leu Leu
242      1140          1145          1150
244 Ser Leu Phe Glu Glu Glu Ile Met Ser Tyr Val Pro Leu Gln Ala Ala
245      1155          1160          1165
247 Phe His Pro Gly Tyr Ser Phe Ser Pro Arg Cys Ser Pro Cys Ser Ser
248      1170          1175          1180
250 Pro Gln Asn Ser Pro Gly Leu Gln Arg Ala Ser Ala Arg Ala Pro Ser
251 1185          1190          1195          1200
253 Pro Tyr Arg Arg Asp Phe Glu Ala Lys Leu Arg Asn Phe Tyr Arg Lys
254      1205          1210          1215
256 Leu Glu Ala Lys Gly Phe Gly Gln Gly Pro Gly Lys Ile Lys Leu Ile
257      1220          1225          1230
259 Ile Arg Arg Asp His Leu Leu Glu Gly Thr Phe Asn Gln Val Met Ala
260      1235          1240          1245
262 Tyr Ser Arg Lys Glu Leu Gln Arg Asn Lys Leu Tyr Val Thr Phe Val
263      1250          1255          1260
265 Gly Glu Glu Gly Leu Asp Tyr Ser Gly Pro Ser Arg Glu Phe Phe Phe
266 1265          1270          1275          1280
268 Leu Leu Ser Gln Glu Leu Phe Asn Pro Tyr Tyr Gly Leu Phe Glu Tyr
269      1285          1290          1295
271 Ser Ala Asn Asp Thr Tyr Thr Val Gln Ile Ser Pro Met Ser Ala Phe
272      1300          1305          1310
274 Val Glu Asn His Leu Glu Trp Phe Arg Phe Ser Gly Arg Ile Leu Gly
275      1315          1320          1325
277 Leu Ala Leu Ile His Gln Tyr Leu Leu Asp Ala Phe Phe Thr Arg Pro
278      1330          1335          1340
280 Phe Tyr Lys Ala Leu Leu Arg Leu Pro Cys Asp Leu Ser Asp Leu Glu
281 1345          1350          1355          1360
283 Tyr Leu Asp Glu Glu Phe His Gln Ser Leu Gln Trp Met Lys Asp Asn
284      1365          1370          1375
286 Asn Ile Thr Asp Ile Leu Asp Leu Thr Phe Thr Val Asn Glu Glu Val
287      1380          1385          1390

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/582,508

DATE: 06/28/2006

TIME: 14:50:13

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06282006\J582508.raw

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289 Phe Gly Gln Val Thr Glu Arg Glu Leu Lys Ser Gly Gly Ala Asn Thr
290      1395      1400      1405
292 Gln Val Thr Glu Lys Asn Lys Lys Glu Tyr Ile Glu Arg Met Val Lys
293      1410      1415      1420
295 Trp Arg Val Glu Arg Gly Val Val Gln Gln Thr Glu Ala Leu Val Arg
296 1425      1430      1435      1440
298 Gly Phe Tyr Glu Val Val Asp Ser Arg Leu Val Ser Val Phe Asp Ala
299      1445      1450      1455
301 Arg Glu Leu Glu Leu Val Ile Ala Gly Thr Ala Glu Ile Asp Leu Asn
302      1460      1465      1470
304 Asp Trp Arg Asn Asn Thr Glu Tyr Arg Gly Gly Tyr His Asp Gly His
305      1475      1480      1485
307 Leu Val Ile Arg Trp Phe Trp Ala Ala Val Glu Arg Phe Asn Asn Glu
308      1490      1495      1500
310 Gln Arg Leu Arg Leu Leu Gln Phe Val Thr Gly Thr Ser Ser Val Pro
311 1505      1510      1515      1520
313 Tyr Glu Gly Phe Ala Ala Leu Arg Gly Ser Asn Gly Leu Arg Arg Phe
314      1525      1530      1535
316 Cys Ile Glu Lys Trp Gly Lys Ile Thr Ser Leu Pro Arg Ala His Thr
317      1540      1545      1550
319 Cys Phe Asn Arg Leu Asp Leu Pro Pro Tyr Pro Ser Tyr Ser Met Leu
320      1555      1560      1565
322 Tyr Glu Lys Leu Leu Thr Ala Val Glu Glu Thr Ser Thr Phe Gly Leu
323      1570      1575      1580

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325 Glu

326 1585

329 <210> SEQ ID NO: 2

330 <211> LENGTH: 6200

331 <212> TYPE: DNA

332 <213> ORGANISM: Homo sapiens

334 <220> FEATURE:

335 <223> OTHER INFORMATION:

W--> 337 <400> 2

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338 gggttttttagg cctggccgcc atggcgctctc cttctagaaa ctcccagagc cgacgcgcggt 60
339 gcaaggagcc gctccgatac agctacaacc cgcaccagtt ccacaacatg gacctcaggg 120
340 gcgcccccca cgatggcgctc accattcccc gctccaccag cgacactgac ctgggtcacct 180
341 cggacagccg ctccacgctc atgggtcagca gctcctacta ttccatcggg cactctcagg 240
342 acctggtcat ccaactgggac ataaaggagg aagtggacgc tggggactgg attggcatgt 300
343 acctcattga tgaggtcttg tccgaaaact ttctggacta taaaaaccgt ggagtcaatg 360
344 gttctcatcg gggccagatc atctggaaga tcgatgccag ctctgacttt gtggaacctg 420
345 aaactaagat ctgcttcaaa tactaccatg gagtgagtg ggccctgcga gcaaccaccc 480
346 ccagtgtcac ggtcaaaaac tcggcagctc ctatttttaa aagcattggg gctgatgaga 540
347 ccgtccaagg acaaggaagt cggaggctga tcagcttctc tctctcagat ttccaagcca 600
348 tgggggttgaa gaaagggatg tttttcaacc cagaccetta tctgaagatt tccattcagc 660
349 ctgggaaaca cagcatcttc ccgcctctcc ctaccatgg acaggagagg agatccaaga 720
350 tcataggcaa caccgtgaac cccatctggc aggcggagca attcagtttt gtgtccttgc 780
351 ccaactgacgt gctggaaatt gaggtgaagg acaagtttgc caagagccgc cccatcatca 840
352 agcgcttctt gggaaagctg tcgatgcccg ttcaaagact cctggagaga cacgccatag 900
353 gggatagggt ggtcagctac acacttggcc gcaggcttcc aacagatcat gtgagtggac 960

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/582,508

DATE: 06/28/2006

TIME: 14:50:14

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06282006\J582508.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25

L:337 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:335



IFWP

RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/582,508

TIME: 11:10:16

Input Set : A:\Sequence Listing - Atty Dkt No 7388-88180.txt

Output Set: N:\CRF4\06212006\J582508.raw

3 <110> APPLICANT: Hisamitsu Pharmaceutical Co., Inc.; Chiba-Prefecture
 5 <120> TITLE OF INVENTION: Method for Determining Clinical Severity of FALS
 7 <130> FILE REFERENCE: FP04-0444-00WO-HM
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/582,508
 C--> 10 <141> CURRENT FILING DATE: 2006-06-09
 12 <150> PRIOR APPLICATION NUMBER: JP 2003-413629
 13 <151> PRIOR FILING DATE: 2003-12-11
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

455 <210> SEQ ID NO: 4
 456 <211> LENGTH: 21
 457 <212> TYPE: DNA
 458 <213> ORGANISM: Artificial Sequence
 460 <220> FEATURE:
 461 <223> OTHER INFORMATION: Primer
 463 <400> SEQUENCE: 4
 464 catgaggta catgccaatc c
 E--> 466 1

Does Not Comply
 Corrected Diskette Needed

(pg. 1)

21

deleted

VERIFICATION SUMMARY

DATE: 06/21/2006

PATENT APPLICATION: US/10/582,508

TIME: 11:10:17

Input Set : A:\Sequence Listing - Atty Dkt No 7388-88180.txt

Output Set: N:\CRF4\06212006\J582508.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25

L:337 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:335

L:466 M:254 E: No. of Bases conflict, this line has no nucleotides.